



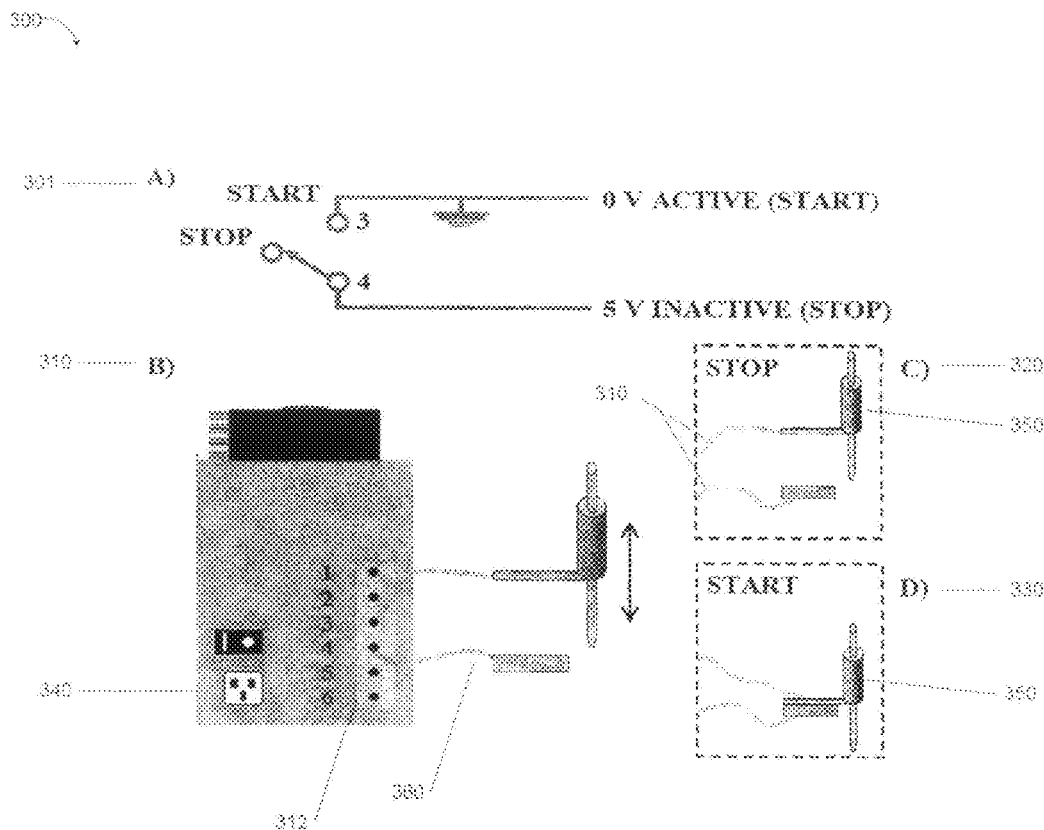
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(19) **United States**(12) **Patent Application Publication**  
**Brennan et al.**(10) **Pub. No.: US 2010/0229999 A1**(43) **Pub. Date: Sep. 16, 2010**(54) **SYSTEM AND METHOD FOR AUTOMATED  
SAMPLE INTRODUCTION**(52) **U.S. Cl. .... 141/1; 141/130**(57) **ABSTRACT**(76) Inventors: **Ryan G. Brennan**, Arlington, VA  
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WASHINGTON,, DC 20036 (US)**(21) Appl. No.: **12/721,452**(22) Filed: **Mar. 10, 2010****Related U.S. Application Data**(60) Provisional application No. 61/158,984, filed on Mar.  
10, 2009, provisional application No. 61/166,189,  
filed on Apr. 2, 2009.**Publication Classification**(51) **Int. Cl.**  
**G01N 35/10** (2006.01)

A method, system and apparatus for an automated sample introduction system, utilizing a demountable direct injection high efficiency nebulizer (d-DIHEN) is provided which incorporates an inductively coupled plasma optical emission spectrometer (ICP-OES) for the measurement of the phosphorus content in acid-digested nucleotides and deoxyribonucleic acid (DNA). The solution uptake rate and volume are reduced from 170  $\mu\text{L min}^{-1}$  to 30  $\mu\text{L min}^{-1}$  and 10 mL to 2.4 mL, respectively, thereby reducing the required DNA sample mass for solutions containing 3  $\mu\text{g}^{-1}$  P from 300  $\mu\text{g}$  to 72  $\mu\text{g}$  DNA, in comparison to previous analyses in our lab using a glass, concentric nebulizer with cyclonic spray chamber arrangement. The use of direct injection also improves P (I) 213.617 nm sensitivity by a factor of 4 on average. A high performance (HP) methodology in combination with the previous sample introduction system and ICP-OES provides simultaneous, time-correlated internal standardization and drift correction resulting in relative expanded uncertainties (% U) for the P mass fractions in the range of 0.1 to 0.4 (95% confidence level) for most of the thymidine 5'-monophosphate (TMP), calf thymus DNA (CTDNA), and plasmid DNA (PLDNA) analyses. The d-DIHEN with HP-ICP-OES methodology allows for the quantification of DNA mass at P mass fractions as low as 0.5  $\mu\text{g g}^{-1}$ , further reducing the required DNA mass to 12  $\mu\text{g}$ , with small uncertainty ( $\leq 0.4\%$ ). The present method, system and apparatus can aid in the development and certification of nucleic acid certified reference materials (CRMs), particularly for these samples that are typically limited in volume.



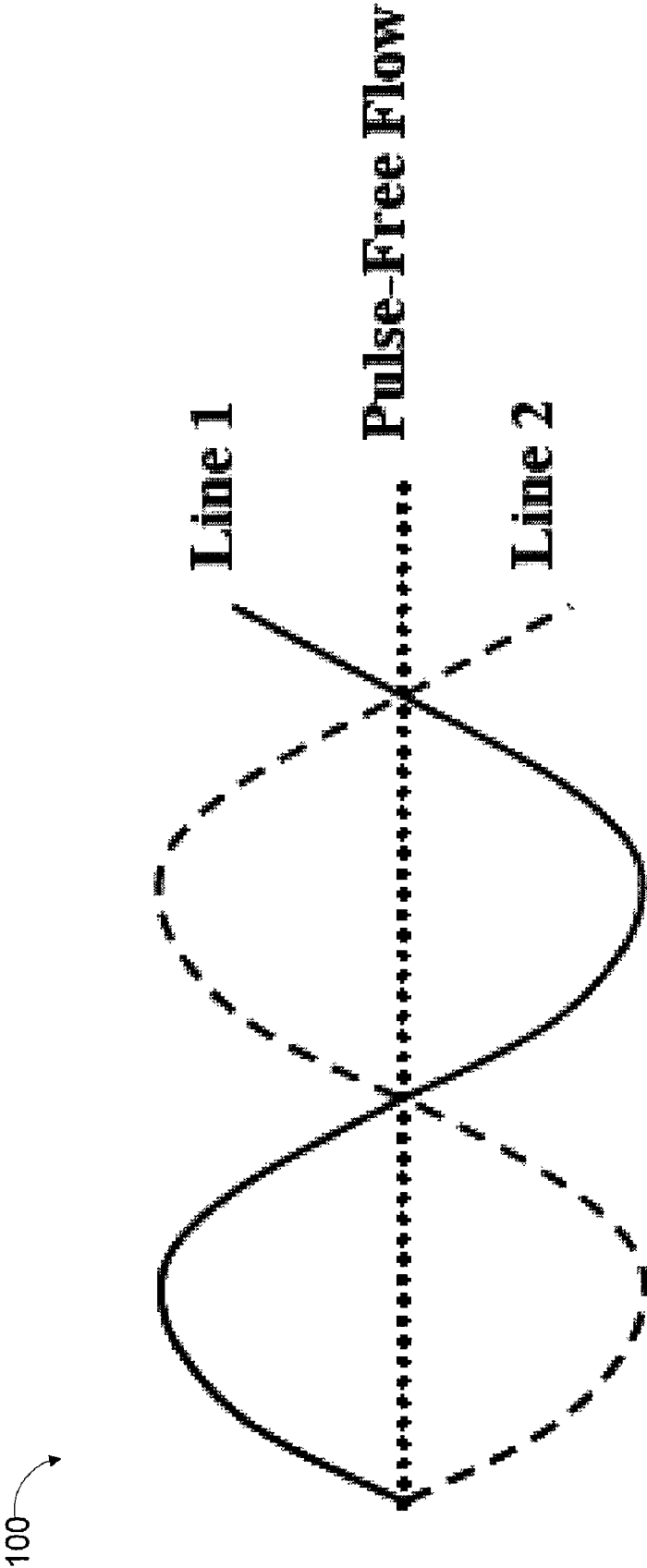


Fig. 1

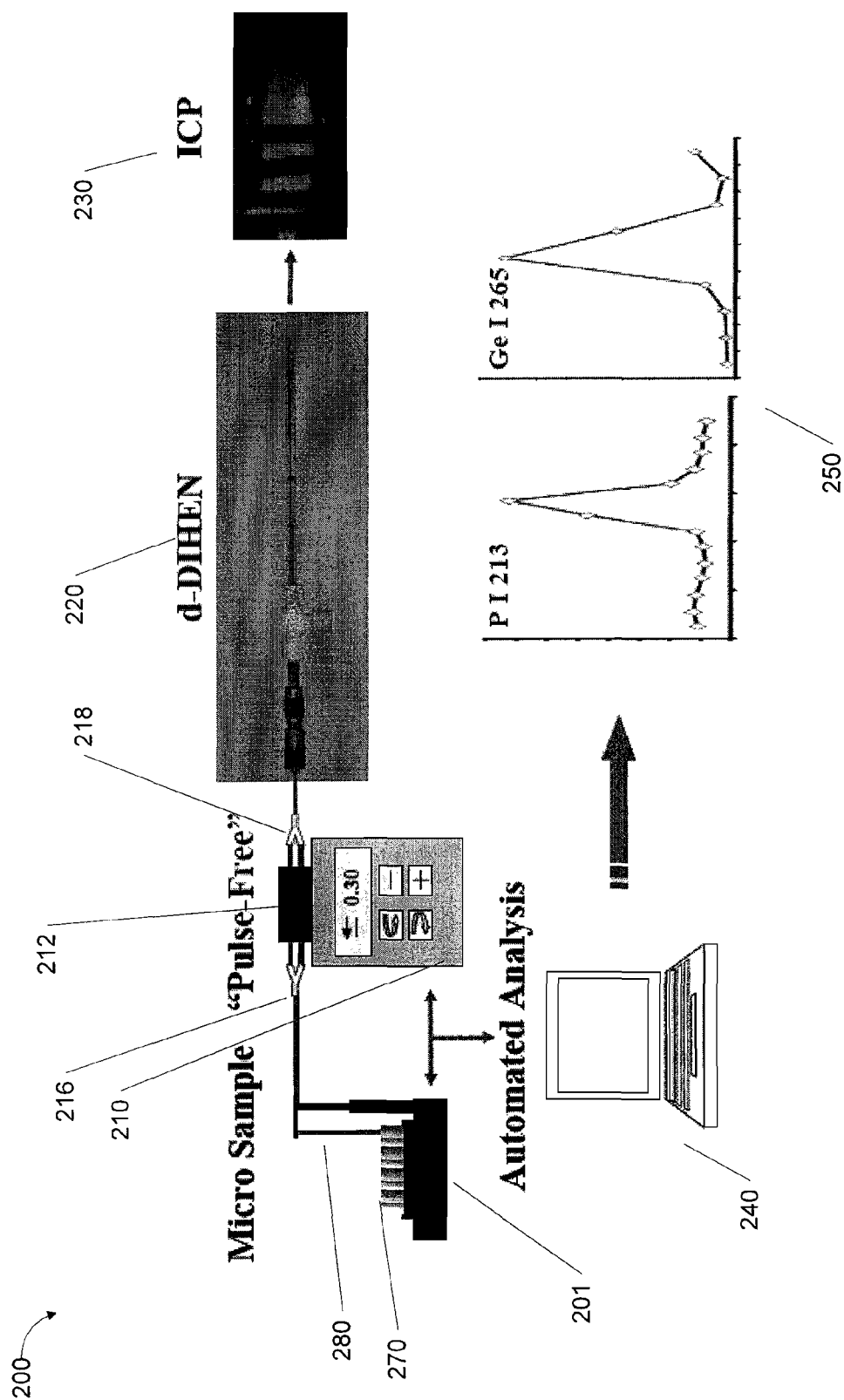
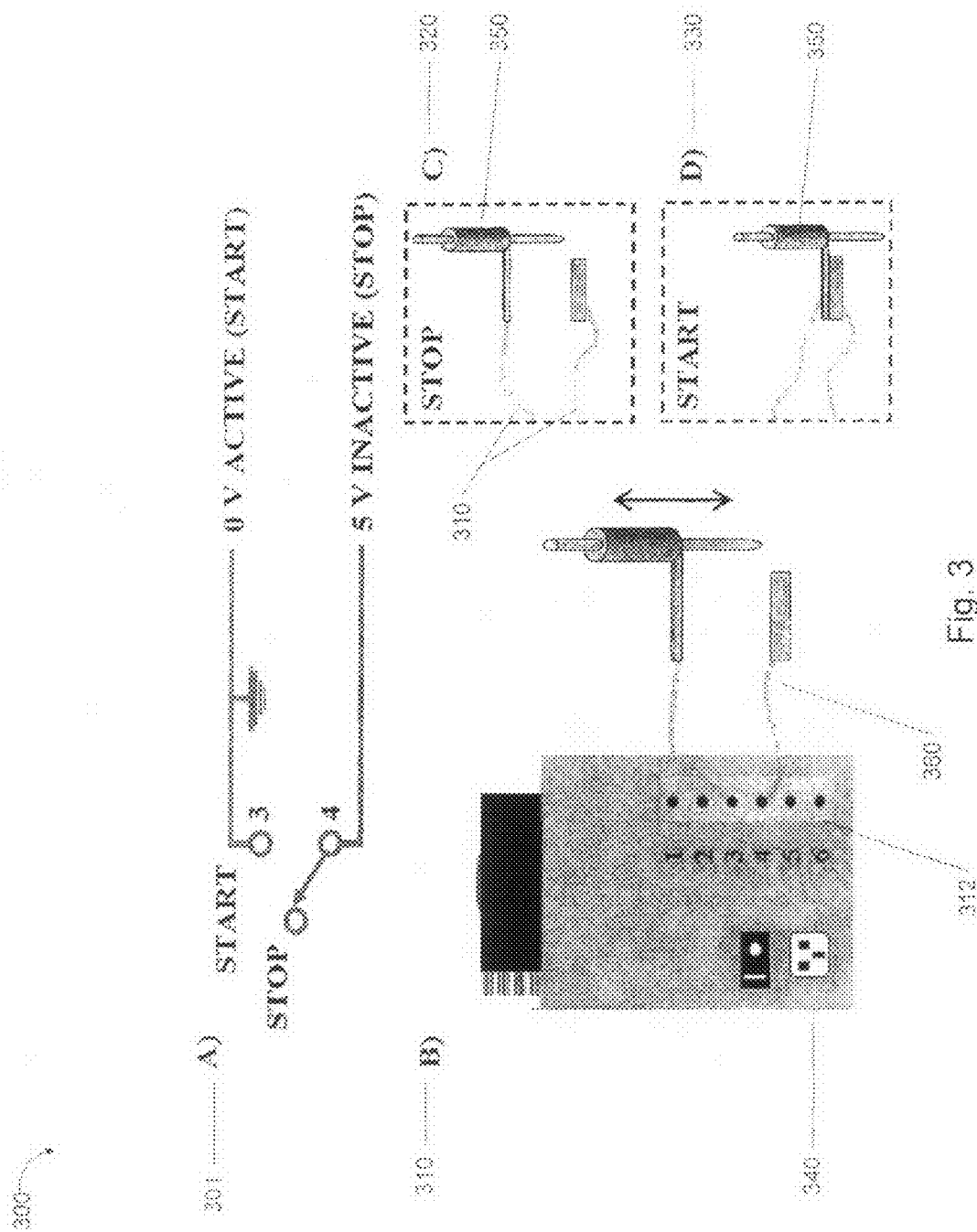


Fig. 2



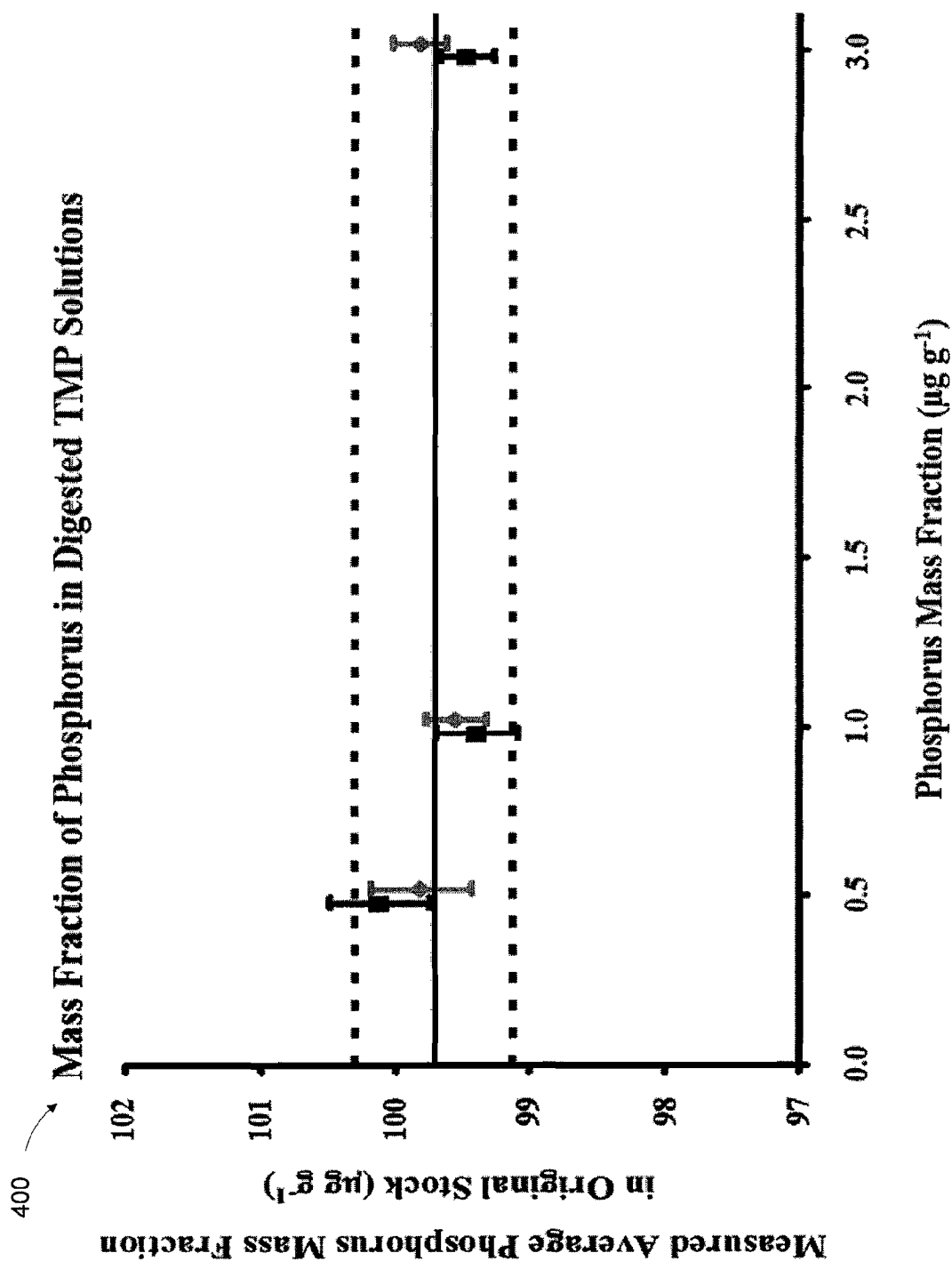


Fig. 4

500 →

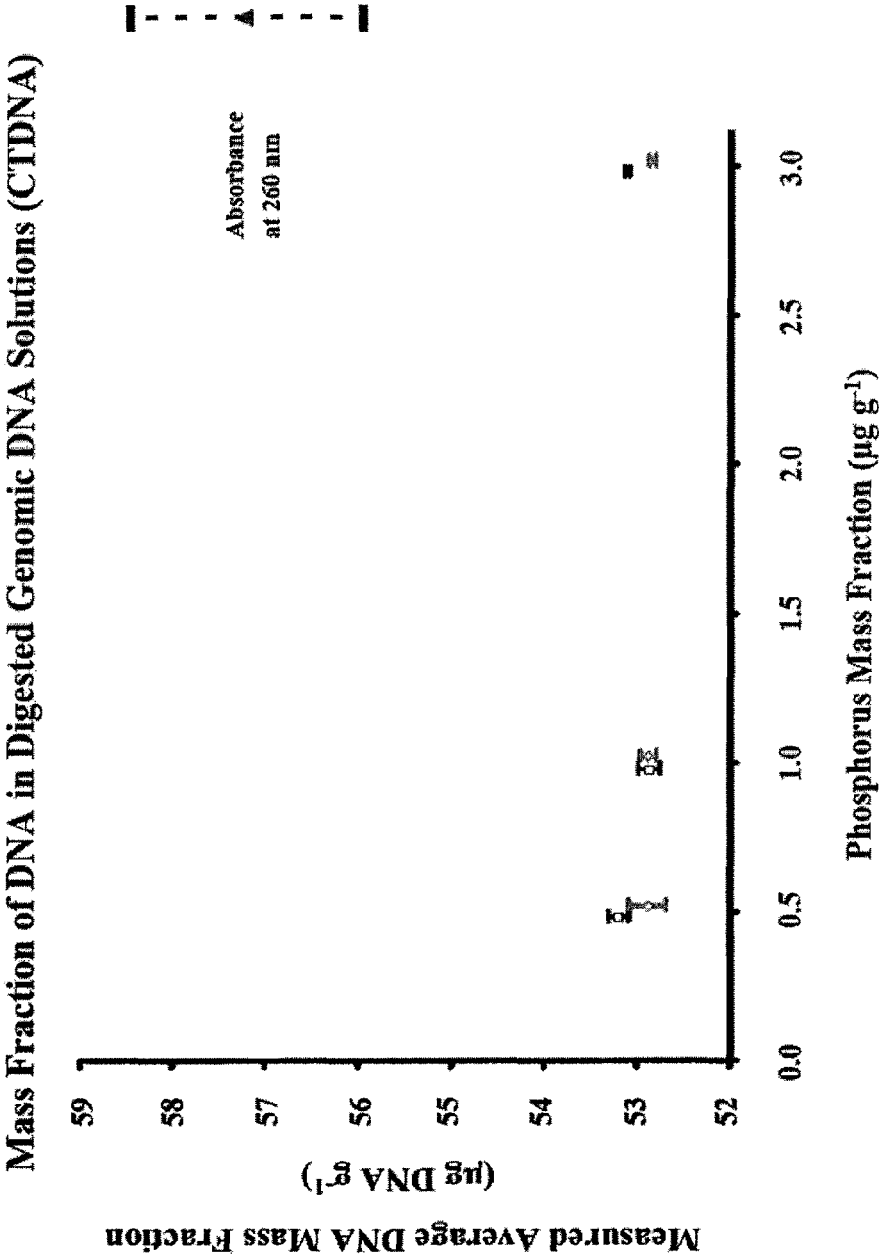


Fig. 5

600

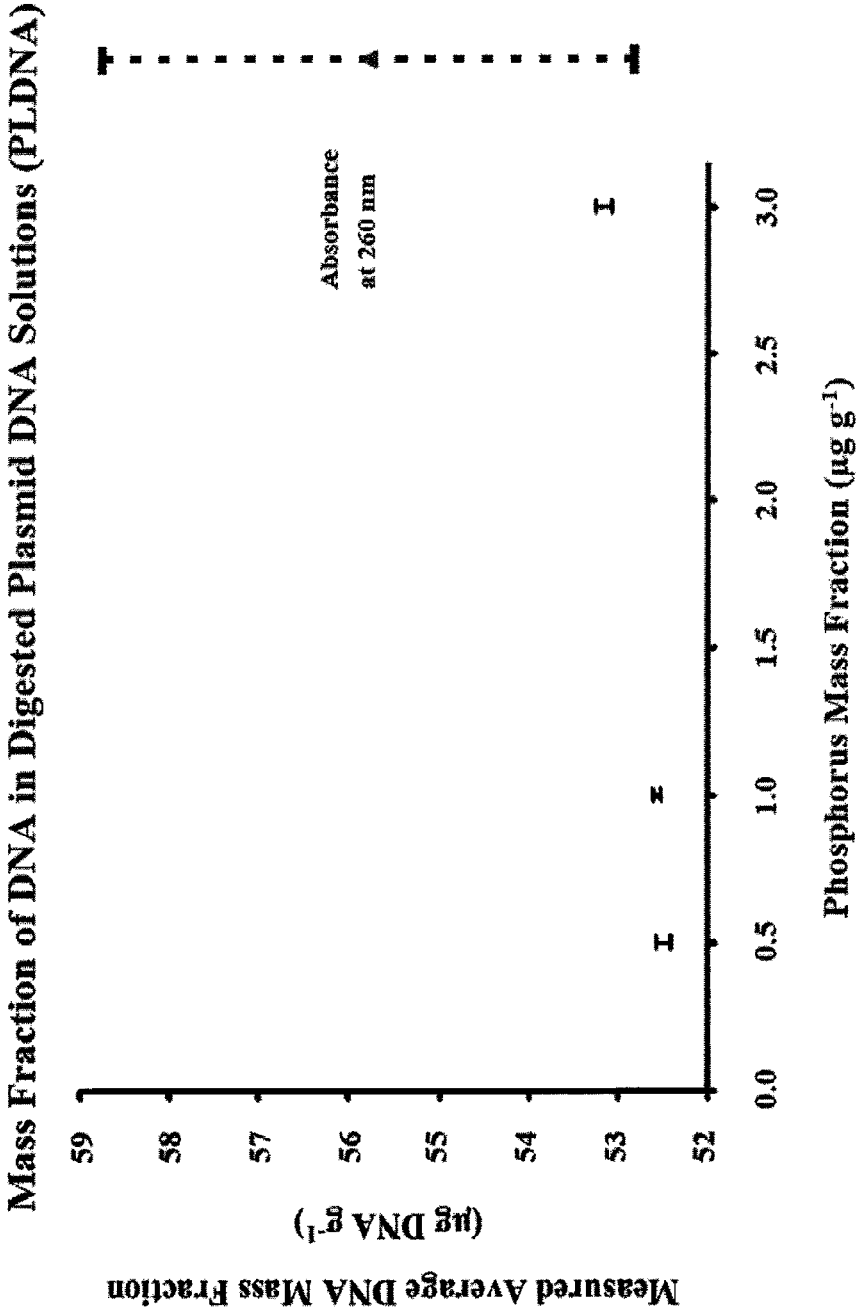


Fig. 6

# SYSTEM AND METHOD FOR AUTOMATED SAMPLE INTRODUCTION

## CROSS-REFERENCE TO RELATED PATENT APPLICATION

[0001] This application claims the benefit under 35 U.S.C. §119(e) of U.S. Provisional Patent Applications No. 61/158,984, filed on Mar. 10, 2009, and No. 61/166,189, filed on Apr. 2, 2009, in the U.S. Patent and Trademark Office, the entire disclosure of each of which is hereby incorporated by reference.

## FIELD OF THE INVENTION

[0002] The present application relates to a system and method for automated sample introduction. Particularly, the present invention provides for an automated sample introduction system, which may be utilized with a demountable direct injection high efficiency nebulizer (d-DIHEN) incorporated with an inductively coupled plasma optical emission spectrometer (ICP-OES) for the measurement of the phosphorus content in acid-digested nucleotides and deoxyribonucleic acid (DNA).

## BACKGROUND OF THE INVENTION

[0003] The present application incorporates by reference, the documents listed as References below, in their entirety, which are referenced throughout the present application as in-line text and as endnotes.

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- [0034] Traditionally, the accurate mass determination of DNA and other nucleic acids is of critical importance in many clinical diagnoses, forensic and molecular biological studies. In addition, these measurements could aid in the determination of transgenic material in agricultural and food products. Because many such commodities are imported and exported annually, they are of great economic and trade interest. European nations require labeling of imported crops and prepared foodstuffs that contain greater than 0.9% transgenic material.1 Such regulations are important to the United States, which is the world's largest exporter of agricultural commodities and prepared foodstuffs with 57.7 million hectares of planted genetically modified (GM) crops (50% of the global area of crops). Many key crops exported from the United States are comprised of transgenic material. For example, of the most voluminous U.S. export crops, 64%, 43%, and 24% of the total global planted soybean, cotton, and corn, respectively, are genetically modified as of 2007.2 For these reasons, the demand has increased for a reliable analysis technique for the development of nucleic acid CRMs.
- [0035] The accurate determination of the amount of DNA isolated from a biological material is not trivial. The results of the more common spectroscopic methodologies to quantify DNA preparations, such as absorbance<sup>3</sup> at 260 nm or fluorescent-dye binding,<sup>4,5</sup> can be seriously compromised by impurities in the DNA preparations or state of the DNA itself. These techniques are also not traceable to the SI because the



calibrations cannot currently be performed using calibration standards whose values are traceable to the SI. Such techniques cannot achieve the high accuracy and precision required to produce CRMs for nucleic acid materials. Quantitative, real-time polymerase chain reaction (Q-PCR) is a powerful technique due to its sensitivity, specificity, and applicability.<sup>6</sup> However, it is imperative that an appropriate amount of template DNA be added to the assay so that trace detection is possible. Overloading the template in the reaction can often interfere with the amplification reaction. Therefore, quantification of total DNA is important, prior to conducting Q-PCR studies.

**[0036]** Inductively coupled plasma mass spectrometry (ICP-MS) offers higher sensitivity and lower detection limits compared to inductively coupled plasma optical emission spectroscopy (ICP-OES), however,<sup>31</sup> P measurements by ICP-MS suffer from interferences ( $^{14}\text{N}^{16}\text{O}^+\text{H}^+$  and  $^{15}\text{N}^{16}\text{O}^+$ ) and incomplete ionization (P has a high first ionization potential  $\sim 10.5$  eV).<sup>7</sup> Other than the use of a collision cell or reaction cell, recent work to overcome such issues utilizes element tagging or nano-particle labeling of nucleic acids and proteins, where a metallic element or metal nano-particle is measured instead of  $^{31}\text{P}$ .<sup>8-11</sup> This concept reported detection limits of  $0.1\text{ ng mL}^{-1}$  to  $0.5\text{ ng mL}^{-1}$  for a target protein with a linear response to protein concentrations over 3 orders of magnitude. More recently, Sharp et al.<sup>12</sup> labeled biotinylated DNA was labeled with a gold nano-particle containing a streptavidin functionality. The labeled DNA was separated and determined by high performance liquid chromatography-ICP-MS (HPLC-ICP-MS). This resulted in a detection limit that would be equivalent to a  $^{31}\text{P}$  detection limit of  $500\text{ pg L}^{-1}$ , had  $^{31}\text{P}$  been measured. With a labeled metal nano-particle, the problems associated with  $^{31}\text{P}$  detection in ICP-MS are eliminated. However, the accuracy of the measurement and enhancement in the analytical sensitivity is dependent on the determination of how many gold atoms have been bound and their locality, because the  $^{197}\text{Au}$  signal is being measured and not  $^{31}\text{P}$ . This area of research is still developing and will be important for quantitative analyses of DNA and nucleic acid samples that require very low detection limits. Bettner et al.<sup>13</sup> achieved precisions lower than 3% for separated DNA fragments with on-line coupling of gel electrophoresis (GE) and ICP-sector field mass spectrometry (ICP-SFMS). However, the accuracy of their method could not be reported due to the lack of CRMs for DNA mass. Evans et al.<sup>14</sup> introduced a potential application of isotopic labeling of peptides with detection by HPLC-ICP-MS. The  $^{151}\text{Eu}$ :  $^{153}\text{Eu}$  isotope ratio was utilized to calculate the original peptide ratio. Peptides were labeled with natural and isotopically enriched  $\text{Eu}^{3+}$ , which enabled the detection and relative quantification of peptides within 5.2% of the known ratio.

**[0037]** Some other traditional approaches to quantify DNA include the use of laser-induced breakdown spectroscopy (LIBS) and an electrochemiluminescence biomarker barcode method. The approach by Le Meur et al.<sup>15</sup> allows for quantification of nucleic acids on a support without labeling using LIBS. This technique lacks sensitivity in comparison to most, but it provides the advantage of avoiding problems associated with attaching fluorophores into nucleic acids. Zhu et al.<sup>16</sup> introduced a PCR-free method to quantitatively detect genetically modified organisms (GMOs) by use of a biomarker barcode method, eliminating the need for PCR amplification which can be time consuming and often leads to false identi-

fication. The authors report high specificity and sensitivity with the ability to detect GMOs from raw material without purification.

**[0038]** A methodology is needed that can be used to provide accurate measurements of DNA and nucleic acid mass that are traceable to the SI providing a CRM for DNA mass. The ICP-OES approach, referred to as high performance ICP-OES (HP-ICP-OES)<sup>17, 18</sup> incorporating a ratio-based technique with drift correction,<sup>19</sup> has been utilized for the measurement of phosphorus content of acid-digested nucleotides and DNA. The HP-ICP-OES measurement of phosphorus provides a highly accurate quantification of mass for both nucleotide monophosphate and DNA with relative uncertainties less than 0.1% (95% confidence level). However, these approaches requires a significant sample size ( $10\text{ mL}$  of a  $3\text{ }\mu\text{g g}^{-1}$  P solution or  $300\text{ }\mu\text{g}$  of DNA), restricting its usefulness for the routine quantification of DNA.<sup>20</sup>

**[0039]** Embodiments of the present invention address at least the drawbacks associated with the conventional art noted above.

#### SUMMARY OF THE INVENTION

**[0040]** As noted above, exemplary embodiments of the present invention address at least the above problems and/or disadvantages, and provide at least the advantages described below.

**[0041]** An exemplary embodiment of the present invention provides a device and methodology that can be utilized for demountable, direct injection high efficiency nebulizer (d-DIHEN)<sup>21,22</sup> to facilitate the introduction of samples into the ICP-OES at low sample uptake rates, limiting sample consumption.

**[0042]** Further, according to an exemplary embodiment of the present invention, the device and methodology can be applicable where the d-DIHEN works with the HP-ICP-OES, the nebulizer aspirates the sample in a "pulse-free" mode and functions with an auto-sampler. Pulse-free aspiration can be achieved using a special pump head that creates opposing pulse patterns in dual sample lines that canceled when the solution lines are combined.

**[0043]** Exemplary embodiments of the present invention provide a micro-switch to halt the peristaltic pump as the sample probe moves from vial to vial, thereby eliminating the introduction of air bubbles that can destabilize the plasma.

**[0044]** Exemplary embodiments of the present invention provide for system and methods where d-DIHEN can operate in a completely automated sampling mode.

**[0045]** According to an exemplary embodiment, with the implementation of the HP-ICP-OES method in combination with the d-DIHEN, the solution uptake rate can be reduced from  $170\text{ min}^{-1}$  to  $30\text{ }\mu\text{L min}^{-1}$ , and the sample size can be reduced from  $10\text{ mL}$  to  $2.4\text{ mL}$ . Consequently with the increase in sensitivity using the d-DIHEN, the required DNA mass for digestion can be reduced from  $300\text{ }\mu\text{g}$  for a  $3\text{ }\mu\text{g g}^{-1}$  P solution to  $12\text{ }\mu\text{g}$  for a  $0.5\text{ }\mu\text{g g}^{-1}$  P solution, while achieving the majority of relative measurement uncertainties on the order of 0.4% or less.

#### BRIEF DESCRIPTION OF THE DRAWINGS

**[0046]** The above and other exemplary features, aspects and advantages of the present invention will become more apparent from the following detailed description of certain

exemplary embodiments thereof when taken in conjunction with the accompanying drawings in which:

**[0047]** FIG. 1 is a schematic block diagram that illustrates how the pulse-free flow rate is achieved for a method, system and apparatus of the present invention, according to an exemplary embodiment.

**[0048]** FIG. 2 is a schematic block diagram that illustrates as exemplary setup for coupling the d-DIHEN to an ICP-OES, for automated, pulse-free analysis associated with a method, system and apparatus of the present invention, according to an exemplary embodiment.

**[0049]** FIG. 3 is a diagram that schematically illustrates and operation of “micro-switch” to allow for automated analysis with the d-DIHEN associated with a method, system and apparatus of the present invention, according to an exemplary embodiment.

**[0050]** FIG. 4 is a schematic block diagram that illustrates ICP-OES measurements of the average P content of the nucleotide TMP compared to the gravimetric value associated with a method, system and apparatus of the present invention, according to an exemplary embodiment.

**[0051]** FIG. 5 is a block diagram that schematically illustrates ICP-OES measurements of the average DNA mass fraction of the prepared genomic DNA (CTDNA) samples compared to the absorbance measurement at 260 nm associated with a method, system and apparatus of the present invention, according to an exemplary embodiment.

**[0052]** FIG. 6 is a schematic block diagram that schematically illustrates ICP-OES measurements of the average DNA mass fraction of the prepared plasmid DNA (PLDNA) samples compared to the absorbance measurement at 260 nm associated with a method, system and apparatus of the present invention, according to an exemplary embodiment.

**[0053]** Throughout the drawings, like reference numerals will be understood to refer to like elements, features and structures.

#### DETAILED DESCRIPTION OF EXEMPLARY EMBODIMENTS

**[0054]** The matters exemplified in this description are provided to assist in a comprehensive understanding of exemplary embodiments of the present invention described with reference to the accompanying drawing figures. Accordingly, those of ordinary skill in the art will recognize that various changes and modifications of the exemplary embodiments described herein can be made without departing from the scope and spirit of the present invention. Also, descriptions of well-known functions and constructions are omitted for clarity and conciseness. Likewise, certain naming conventions, labels and terms as used in the context of the present disclosure are, as would be understood by skilled artisans, non-limiting and provided only for illustrative purposes to facilitate understanding of certain exemplary implementations of the embodiments of the present invention.

**[0055]** Exemplary embodiments of the present invention provide a demountable, direct injection high efficiency nebulizer (d-DIHEN) that can be utilized to facilitate the introduction of samples into the ICP-OES at low sample uptake rates, limiting sample consumption.

**[0056]** Further, according to an exemplary embodiment of the present invention, where the d-DIHEN works with the HP-ICP-OES, the nebulizer aspirates the sample in a “pulse-free” mode and functions with an auto-sampler. Pulse-free aspiration can be achieved using a special pump head that

created opposing pulse patterns in dual sample lines that canceled when the solution lines were combined.

**[0057]** As shown in FIGS. 1-6, exemplary embodiments of the present invention provide for a micro-switch 360 to halt the peristaltic pump 210, 340 as a sample probe 280, 350 moves from vial to vial 270, thereby eliminating the introduction of air bubbles that can destabilize the plasma. Exemplary embodiments of the present invention provide for the d-DIHEN operating in a completely automated sampling mode. With the implementation of the HP-ICP-OES method in combination with the d-DIHEN, the solution uptake rate can be reduced from 170  $\mu\text{L min}^{-1}$  to 30  $\mu\text{L min}^{-1}$ , and the sample size can be reduced from 10 mL to 2.4 mL. Consequently with the increase in sensitivity using the d-DIHEN, the required DNA mass for digestion can be reduced from 300  $\mu\text{g}$  for a 3  $\mu\text{g g}^{-1}$  P solution to 12  $\mu\text{g}$  for a 0.5  $\mu\text{g g}^{-1}$  P solution, while achieving the majority of relative measurement uncertainties on the order of 0.4% or less.

**[0058]** Preparation of Nucleotides and Nucleic Acids

**[0059]** According to an exemplary embodiment of the present invention, the nucleotide monophosphate, genomic DNA, and plasmid DNA are thymidine 5'-monophosphate (TMP), deoxyribonucleic acid sodium salt from calf thymus (CTDNA), and a plasmid (pPCR Script Amp, Stratagene) propagated in *Escherichia coli* (PLDNA), respectively. The TMP and CTDNA can be obtained from Sigma Chemical Co. (T-9758 and D1501). According to an exemplary embodiment, samples can be stored in 1 mM TRIS buffer (pH 8) and 5% HCl (v/v).<sup>20</sup>

**[0060]** Phosphorus Measurements—ICP-OES

**[0061]** Traditionally, HP-ICP-OES<sup>17-19</sup> was used to determine the phosphorus mass fraction with an internal standard spike of Ge to help correct for high-frequency noise, and a drift correction procedure to correct for low-frequency noise (i.e., drift). Any observed difference between the sample and calibration standard is used to compute the phosphorus mass fraction in the sample. This calculation is described by the following equation:<sup>19</sup>

$$P \text{ mass fraction } (\mu\text{g g}^{-1}) = \left( \frac{\left( \frac{I_P}{I_{Ge}} \right)_{\text{Unknown}}}{\left( \frac{I_P}{I_{Ge}} \right)_{\text{Calibrant}}} \right) * \left( \frac{\left( \frac{m_P}{m_{Ge}} \right)_{\text{Calibrant}}}{\left( \frac{m_P}{m_{Ge}} \right)_{\text{Unknown}}} \right) \quad (1)$$

**[0062]** where I is the signal intensity and m is the mass of the P or Ge in the calibrant and unknown solutions. The calibration relationship between the signal intensity ratio and the mass ratio is linear with an intercept of zero as long as the blank and background are appropriately corrected for in the signal intensity ratio. The HP-ICP-OES method was utilized due to its ability to provide elemental determinations with relative expanded uncertainties (% U) that are better than a few parts per thousand (95% confidence level).<sup>12-19</sup>

**[0063]** An Optima 5300 DV ICP-OES instrument (for example, an Optima 5300 DV ICP-OES instrument can be used for these determinations with the operating conditions listed in Table 1 (as illustrated below).

TABLE 1

Operating Conditions for Ar ICP-OES	
ICP-OES System	PE Optima 5300 DV
Power (kW)	1.5
Plasma gas (L min <sup>-1</sup> )	15
Auxiliary gas (L min <sup>-1</sup> )	0.5
Nebulizer gas (L min <sup>-1</sup> )	0.13
Viewing	axial
Sample uptake (μL min <sup>-1</sup> )	30
Analyte wavelength (nm)	P I 213.617
Reference wavelength (nm)	Ge I 265.118
On-chip integration time (s)	1.024 or 2.048
Total read time (s)	8.192

**[0064]** Under these conditions, a robust plasma can be formed with a Mg (II) 280.270 nm/Mg (I) 285.213 nm intensity ratio on the average of 9.2. This value can be corrected for the differing Echelle grating diffraction efficiencies at the two wavelengths by multiplying the observed ratio (5.0) by 1.85.<sup>23</sup> The selection of the P (I) 213.617 nm and Ge (I) 265.118 nm lines can be due to similar excitation energies and the observed intensity ratio precision (% RSD). The ratio RSDs (repeatability) ranged from 1.5% to 0.2% (based upon 5 replicates) for 0.5 μg g<sup>-1</sup> P to 3.0 μg g<sup>-1</sup> P, respectively. The best RSDs are achieved for 3 μg g<sup>-1</sup> P (0.2% to 0.4%) due to the larger signal intensity (larger S/N) observed in comparison to 0.5 μg g<sup>-1</sup> P. A segmented-array, charge-coupled device detector can be used for signal integration. The integration parameters were set manually for each P/Ge mass fraction ratio to provide simultaneous acquisition of the signal.

**[0065]** To reduce solution uptake rate and sample size, a d-DIHEN can be utilized with critical dimensions (see Table 2, as illustrated below) successful in a previous work with similar challenges.<sup>24</sup>

TABLE 2

Critical dimensions for d-DIHEN	
Solution capillary i.d. (μm)	75
Capillary wall thickness (μm)	12
Solution capillary o.d. (μm)	138
Gas nozzle orifice i.d. (μm)	150

**[0066]** A micro-auto-sampler (for example, a CETAC ASX-100 micro-auto-sampler) can be used with a peristaltic pump (for example, a Gilson Miniplus-3 peristaltic pump) for micro-sample automation and solution delivery. To improve precision, a pump head **212** (for example, a Spetec Perimax 16/2 Antipuls pump head) was installed onto the pump **210** to deliver a “pulse-free” solution flow rate (Spetec GmbH, Erding, Germany). The pulsation that is commonly observed with the use of a peristaltic pump is eliminated through the use of double-stranded pump tubing and the phase displaced roller head of the pump (for example a Spetec Perimax 16/2 pump head). The solution uptake is split in two by a y-connector **216** to construct the double-stranded pump tubing, allowing each solution line to pass over separate sets of rollers that are offset from each other.

**[0067]** FIG. 1 is a schematic block diagram that illustrates how the “pulse-free” flow rate is achieved associated with a method, system and apparatus of the present invention, according to an exemplary embodiment **100**. The wave peak in one solution line coincides with the wave trough in the other line, so that the peaks and troughs cancel each other out,

thus the phase displaced solution uptake eliminates any fluctuations. This action provides a “pulse-free” flow as the two solution lines are recombined together with another y-connector **218** downstream from the roller head.

**[0068]** FIG. 2 is a schematic block diagram that illustrates typical setup for coupling the d-DIHEN **220** to an ICP-OES **230** (for example, a PerkinElmer Optima 5300 DV ICP-OES), for automated **240**, pulse-free analysis associated with a method, system and apparatus of the present invention, according to an exemplary embodiment **200**, **250**.

**[0069]** Since the introduction of the DIHEN series,<sup>21,22,25,26</sup> no attempts to automate sample delivery with these nebulizers have been reported. One of the main disadvantages of automation with these nebulizers is the introduction of air bubbles in the solution line that could extinguish the plasma in most ICP instruments.

**[0070]** According to an exemplary embodiment of the present invention as illustrated in FIG. 2, an external peristaltic pump **210** which can be used to provide pulse-free aspiration utilizing a micro-switch **360** fabricated from copper foil, to control the operation of the peristaltic pump **210** via the positioning of the sample probe **280** on the micro-auto-sampler. The switch **360** can be constructed by connecting two wires **310** from a copper contact on the sample probe to the peristaltic pump Start/Stop contacts (pins **3** and **4**). The switch could then be closed **330** (pump started) when the auto-sampler probe **350** is lowered and opened **320** (pump stopped) when the probe **350** is raised (FIG. 3). The micro-switch **360** prevents an air bubble from being introduced into the solution line when the micro-auto-sampler probe **350** moves from one sample vial **270** to the next. According to exemplary embodiments, the present invention provides for an automated procedure developed for use with the d-DIHEN **220**, without plasma shutdowns.

**[0071]** FIG. 3 is a diagram that illustrates a schematic and operation of “micro-switch” to allow for automated analysis with the d-DIHEN associated with a method, system and apparatus of the present invention, according to an exemplary embodiment **300**. According to an exemplary embodiment of the present invention, the schematic and operation illustrate: A) Electrical control diagram **301**; B) a peristaltic pump **310**, **340** with 6-pin barrier strip **312** (for example, a Gilson minipuls-3 peristaltic pump); C) a micro-switch **360** with auto-sampler probe **350** in “STOP” position **320**; and D) micro-switch with auto-sampler probe **350** in “RUN” (or “START”) position **330**. An exemplary embodiment of the present invention provides a micro-switch **360** to halt the peristaltic pump **310** as the sample probe **280**, **350** moves from vial to vial **270**, thereby eliminating the introduction of air bubbles that can destabilize the plasma.

**[0072]** According to exemplary embodiments of the present invention, four solutions can be prepared gravimetrically from stock solutions for both the calibration standards and nucleic acid samples (TMP, CTDNA, and PLDNA). The TMP and CTDNA sample stock solutions, not limited by sample volume like PLDNA, can be each subdivided into two solutions (TMP (1), TMP (2), CTDNA (1), and CTDNA (2)) for a means of comparison. Exemplary embodiments of the present invention can be diluted and analyzed at various mass fractions. For example, three embodiments of the present invention can exemplify implementations for three different P mass fractions (0.5 μg g<sup>-1</sup> to 1.0 μg g<sup>-1</sup>, and 3.0 μg g<sup>-1</sup>), where the calibrants can be matched very closely in P mass fraction and matrix to that of the samples. The sample and calibrant

solutions can also be spiked with a Ge solution with a mass fraction of  $10 \mu\text{g g}_{-1}$  to obtain a final Ge mass fraction of  $0.5 \mu\text{g g}_{-1}$  to  $1.0 \mu\text{g g}_{-1}$  (depending on the P mass fraction analyzed). Phosphorus calibration standards can be prepared from NIST SRM 194 (Ammonium Dihydrogen Phosphate) with the internal standard solution from a  $10,000 \mu\text{g mL}^{-1}$  Ge CRM solution. A single determination can comprise five repeat measurements (in random order), requiring approximately 6 h to 9 h to complete each analysis. Determinations at  $0.5 \mu\text{g g}_{-1}$  P,  $1.0 \mu\text{g g}_{-1}$  P, and  $3.0 \mu\text{g g}_{-1}$  P can each be analyzed twice (except for PLDNA at  $3 \mu\text{g g}_{-1}$  P) to calculate the average P mass fraction for a given sample in the original stock. All solutions can be prepared in analytical grade 2%  $\text{HNO}_3$  (v/v) and a 1 mM TRIS buffer.

[0073] According to exemplary embodiments of the present invention, as a means of method validation, the P content of TMP can be measured both by HP-ICP-OES and gravimetry. The P mass fractions observed using HP-ICP-OES can be within 0.11% to 0.42% of the gravimetric value. As a result, the analyses of TMP by HP-ICP-OES can be considered successful, and the TMP can be further utilized as a control in the analyses of the CTDNA and PLDNA. For the DNA analyses, the HP-ICP-OES P mass fractions for the TMP can be within 0.18% to 0.96% of the gravimetric value. The values were considered to be in control as they are within the uncertainty range of the gravimetric value.

[0074] Measurement Uncertainties

[0075] According to exemplary embodiments of the present invention, uncertainties shown for the data consist of expanded uncertainties expressed at the 95% level of confidence and are calculated according to the principles of the *ISO Guide to the Expression of Uncertainty in Measurement* (GUM).<sup>27</sup> Expanded uncertainties were determined for ICP-OES phosphorus measurements as well as the gravimetric preparations of TMP by using the following equations:

$$u_c = \sqrt{u_1^2 + u_2^2 + u_3^2 + \dots} \quad (2)$$

$$U = k u_c \quad (3)$$

$$\% U = \frac{U}{x} * 100 \quad (4)$$

[0076] Where  $u_i$  represents the individual component of uncertainty,  $u_c$  is the combined uncertainty,  $k$  is the expansion factor based on the Student's  $t$  for the chosen level of confidence,  $U$  is the expanded uncertainty, and  $x$  is the observed measurement of P or TMP mass. Propagated components of uncertainty include observed measurement repeatability, observed variability in the determination of ICP-OES sensitivity, and uncertainties in the known values for the calibration standards. Uncertainties in the gravimetric preparation of TMP include those associated with the mass of TMP, the mass of the 5% HCl solution, Karl Fischer determination of the water content of TMP, and possible undetected TMP impurities.<sup>20</sup> The absorbance measurements for the plasmid and calf thymus DNA can be made on a Beckman DU-650 spectrophotometer using a quartz cuvet. The expanded uncertainties are based on the measured standard uncertainty where the coverage factor  $k=4.3$ .

## RESULTS AND DISCUSSION

[0077] According to exemplary embodiments of the present invention, The DIHEN and d-DIHEN, compared to the conventional nebulizer-spray chamber arrangement, offer at least the following benefits: (1) 100% sample transport efficiency; (2) a low internal dead volume and thus rapid response times and reduced memory effects; (3) improved precision by eliminating noise sources attributed to the spray chamber; and (4) similar or improved detection limits and sensitivity when operated at  $\mu\text{L min}_{-1}$  sample uptake rates.

[0078] FIG. 4 is a schematic block diagram that illustrates ICP-OES measurements of the average P content of the nucleotide TMP compared to the gravimetric value associated with a method, system and apparatus of the present invention, according to an exemplary embodiment 400.

[0079] According to an exemplary embodiment of the present invention, TMP samples were analyzed at three different P mass fractions, (1)  $0.5 \mu\text{g g}_{-1}$ , (2)  $1.0 \mu\text{g g}_{-1}$ , and (2)  $3.0 \mu\text{g g}_{-1}$  P, in two trials; square—TMP (1) and diamond—TMP (2). Each trial represents the average of two experiments. Please note that the data points are offset from the x-axis value only to allow the error bars from each trial to be observed. The relative expanded uncertainties (% U) for all the TMP analyses are represented by the error bars (95% confidence level). The solid line represents the P gravimetric value, with the dashed lines representing the measurement uncertainty of the gravimetric value.

[0080] Further, FIG. 4 illustrates exemplary embodiments of the present invention illustrating measurements of the average P content of the nucleotide TMP, one of the four common base components of DNA. The TMP samples were analyzed at three different P mass fractions,  $0.5 \mu\text{g g}_{-1}$ ,  $1.0 \mu\text{g g}_{-1}$ , and  $3.0 \mu\text{g g}_{-1}$  P to determine the effects on accuracy and precision as the P mass fraction was varied. The ICP-OES measured average P mass fraction in the TMP original stock solution is virtually the same for both TMP (1) and TMP (2) at each mass fraction, thus providing method validation. The relative expanded uncertainties for all the TMP analyses ranged from 0.20% to 0.38%. In comparison to the results using our previous sample introduction system, the expanded uncertainties are slightly larger for the d-DIHEN. Also, the expanded uncertainties increase as the sample P mass fractions decrease. However, these increases are more than acceptable for accurate determinations of P in this material. As a result, limited samples, previously analyzed near  $3 \mu\text{g g}_{-1}$  P, can be increased through dilution (a factor of  $\sim 10$  in this case). Finally, the differences between the d-DIHEN-HP-ICP-OES values for the P mass fraction and those from the gravimetric measurement ranged from 0.11% to 0.42%. These results are comparable to or better than previous results<sup>20</sup> (without d-DIHEN technology) demonstrating a consistent correlation between ICP-OES measurements, regardless of the sample introduction system, and gravimetric measurements.

[0081] Determinations of the average mass fractions of phosphorus in CTDNA and PLDNA are illustrated in FIGS. 5 and 6, according to exemplary embodiments of the present invention.

[0082] FIG. 5 is a schematic block diagram that illustrates ICP-OES measurements of the average DNA mass fraction of the prepared genomic DNA (CTDNA) samples compared to the absorbance measurement at 260 nm associated with a method, system and apparatus of the present invention, according to an exemplary embodiment 500. According to an

exemplary embodiment of the present invention, the CTDNA samples were analyzed at three different P mass fractions, (1)  $0.5 \mu\text{g g}_{-1}$ , (2)  $1.0 \mu\text{g g}_{-1}$ , and (2)  $3.0 \mu\text{g g}_{-1}$  P, in two trials; square—CTDNA (1) and diamond—CTDNA (2). Each trial represents the average of two experiments. The data points are offset from the x-axis value only to allow the error bars from each trial to be observed. The relative expanded uncertainties (% U) for all the CTDNA analyses are represented by the error bars (95% confidence level). The triangle represents the DNA mass fraction determined by the absorbance measurement at 260 nm, with the dashed error bar representing the measurement uncertainty.

**[0083]** FIG. 6 is a schematic block diagram that illustrates ICP-OES measurements of the average DNA mass fraction of the prepared plasmid DNA (PLDNA) samples compared to the absorbance measurement at 260 nm associated with a method, system and apparatus of the present invention, according to an exemplary embodiment of the present invention **600**.

**[0084]** According to an exemplary embodiment of the present invention, the PLDNA samples were analyzed at three different P mass fractions,  $0.5 \mu\text{g g}_{-1}$ ,  $1.0 \mu\text{g g}_{-1}$ , and  $3.0 \mu\text{g g}_{-1}$  P. Each value represents the average of two experiments, except for  $3.0 \mu\text{g g}_{-1}$ , which was a single experiment. The relative expanded uncertainties (% U) for all the PLDNA analyses are represented by the error bars (95% confidence level). The triangle represents the DNA mass fraction determined by the absorbance measurement at 260 nm, with the dashed error bar representing the measurement uncertainty.

**[0085]** Further, FIGS. 5 and 6 illustrate exemplary embodiments of the present invention relating to three different P mass fraction levels. The ICP-OES measured P mass fractions for all the DNA analyses are in very good agreement with each other. The calculated DNA mass shows reasonable relative expanded uncertainties overall (0.12% to 0.42%) with 0.75% being the highest for the analysis of one of the sets of CTDNA samples. Reduction of the required sample size with the use of the d-DIHEN can be utilized for the analysis of the PLDNA that was previously limited to a single experiment per sample. The ICP-OES measurements are consistently 8% and 6% lower than the absorbance measurement of DNA mass for the CTDNA and PLDNA, respectively.

**[0086]** Previously, a negative bias with respect to absorbance was also observed for CTDNA and PLDNA, 8% and 10%, respectively without using the d-DIHEN. According to exemplary embodiments of the present invention, a negative bias (–) can be preferred because a positive bias of the DNA mass fraction could arise from impurities (phosphorus containing molecules) present in the samples or contamination during the sample analysis, thereby overestimating the mass fraction of CTDNA and PLDNA. English et al.<sup>28</sup> compared ICP-OES measurements to four other quantification methods for DNA mass and reported biases of –8% to 38%.

**[0087]** According to exemplary embodiments of the present invention, an improvement in measurements can be attributed to the use of the absorbance value of alkali denatured DNA and the use of the extinction coefficient for single stranded DNA versus the extinction coefficient for double stranded DNA.<sup>29</sup> The smaller uncertainty observed in the absorbance measurement of the CTDNA versus that of the PLDNA (FIGS. 5 and 6) can be the result of sample preparation. Variability in the dilution of the PLDNA samples with NaOH could have occurred. The use of a method such as HP-ICP-OES in the development of CRMs for DNA mass can

lead to an increase in the accuracy. A more precise and accurate quantification of DNA may be of value to revisit the issue of the extinction coefficient for DNA, that was determined in 1948 by Chargaff and Zamenhof.<sup>30</sup>

**[0088]** According to exemplary embodiments of the present invention, the results of the analysis of TMP, CTDNA, and PLDNA are reproducible with reasonable expanded uncertainties regardless of using the previous setup or the d-DIHEN. Exemplary embodiments of the present invention provide for an automated process for methods necessitating small sample size and reduced solution flow rates, while being able to utilize all the aforementioned benefits of the d-DIHEN. The micro-switch and pulse-free flow create a more user friendly d-DIHEN and increase the potential for the d-DIHEN to be used more widely. With this setup (FIG. 1), the solution uptake rate was reduced from  $170 \mu\text{L min}_{-1}$  to  $30 \mu\text{L min}_{-1}$  and the required sample size was reduced from 10 mL to 2.4 mL. Additionally, the 4-fold increase in the P (I) 213.617 nm sensitivity allowed for a decrease in the P mass fraction ( $3 \mu\text{g g}_{-1}$  to  $0.5 \mu\text{g g}_{-1}$ ) analyzed and DNA mass consumed ( $300 \mu\text{g}$  to  $12 \mu\text{g}$ ) compared to a glass concentric nebulizer with cyclonic spray chamber arrangement.

**[0089]** Exemplary embodiments of the present invention provide for analysis of the TMP, CTDNA, and PLDNA without the use of the TRIS buffer. The TRIS buffer helps to keep the nucleotide and DNA stable in the solution prior to analysis; however, a factor of 2 reduction in sensitivity is observed, compared to samples using only a 2%  $\text{HNO}_3$  (v/v) matrix. Even with this reduction, the current setup with the use of the d-DIHEN offers improvement compared to the traditional sample introduction system, considering the solution flow rate, material required, and the increase in P (I) 213.617 nm sensitivity. Without the TRIS buffer, exemplary embodiments of the present invention provide accurate quantification of phosphorus with small uncertainty at mass fractions potentially as low as  $0.1 \mu\text{g g}_{-1}$  (2.4  $\mu\text{g}$  DNA).

**[0090]** Exemplary embodiments of the present invention provide for an automated sample analysis system, utilizing the d-DIHEN, for ICP-OES was successfully incorporated for the accurate measurement of the phosphorus content of acid-digested nucleotides and DNA with small uncertainty. The solution uptake rate can be reduced, as observed in our previous analyses, from  $170 \mu\text{L min}_{-1}$  to  $30 \mu\text{L min}_{-1}$  and the required sample size was reduced from 10 mL to 2.4 mL, while providing relative expanded uncertainties (% U) in the range of 0.1 to 0.4 (95% confidence interval) for most of the TMP, CTDNA, and PLDNA analyses. The use of direct injection improves P (I) 213.617 nm sensitivity by a factor of 4 on average compared to a glass concentric nebulizer with cyclonic spray chamber arrangement, permitting the consumption of 12  $\mu\text{g}$  of DNA analyzing a  $0.5 \mu\text{g g}_{-1}$  P solution. Exemplary embodiments of the present invention provide at least for the benefit of aiding in the development of certified reference materials (CRMs) with nucleic acid content, particularly for samples that are typically limited in volume.

**[0091]** Although exemplary embodiments of the present invention have been disclosed for illustrative purposes, those skilled in the art will appreciate that various modifications, additions, and substitutions are possible, without departing from the scope of the present invention. Therefore, the present invention is not limited to the above-described embodiments, but is defined by the following claims, along with their full scope of equivalents.

What is claimed is:

1. A method for automated sample introduction, the method comprising:

positioning a sample probe for retrieving a sample from a plurality of sample containers;

controlling a pump based on the positioning of the sample probe with respect to the sample containers; and

providing pulse-free aspiration of the sample by pumping action of the pump,

wherein the providing of the pulse-free aspiration comprises utilizing a micro-switch to control the pump to stop the pumping action when the sample probe is not positioned to retrieve the sample from at least one of the plurality of sample containers.

2. The method of claim 1, wherein the micro-switch controls starting and stopping operations of the pump based on positioning of the sample probe relative to the sample containers to retrieve the sample when the probe is positioned to retrieve the sample from at least one of the plurality of sample containers as the sample probe moves amongst the plurality of containers.

3. The method of claim 1, wherein each of the plurality of sample containers comprises a vial.

4. A system for automated sample introduction, the system comprising:

a sample probe for retrieving a sample from a plurality of sample containers;

a pump for providing pulse-free aspiration of the sample retrieved from at least one of the sample containers by pumping action of the pump; and

a controller for controlling the pumping action based on positioning of the sample probe with respect to at least one of a plurality of sample containers,

wherein the controller controls the pump to stop the pumping action when the sample probe is not positioned to retrieve the sample from at least one of the plurality of sample containers.

5. The method of claim 4, wherein each of the plurality of containers comprises a vial.

6. The system of claim 4, wherein the pump creates opposing pulse patterns in dual sample lines that transport samples therethrough that cancel when the solution lines are combined.

7. The system of claim 6, wherein the dual sample lines comprise a first y-connector creating a double-stranded pump tubing for allowing each solution line to pass over separate sets of rollers that are offset from each other, and comprising a second y-connector downstream from the roller head recombining the solution lines.

8. An apparatus for automated sample introduction, the apparatus comprising:

a micro-switch;

a sample probe for retrieving a sample solution from a plurality of sample containers; and

a pump for providing pulse-free aspiration of the sample solution by pumping action,

wherein the micro-switch controls the pump to stop the pumping action when the sample probe is not positioned to retrieve the sample from at least one of the plurality of sample containers.

9. The apparatus of claim 8, wherein the micro-switch comprises a plurality of wires configured to form an electrical connection when the sample probe is positioned to retrieve the sample from at least one of the plurality of sample containers.

10. The apparatus of claim 8, wherein the plurality of wires comprise at least a first portion configured on the sample probe and a second portion configured with respect to the at least one of the plurality of sample containers whereby the electrical connection is formed when the sample probe is positioned to retrieve the sample and broken when the probe is positioned where the probe cannot retrieve the sample.

11. The method of claim 8, wherein each of the plurality of containers comprises a vial.

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